

0272wo310\_v2\_ST25.txt  
SEQUENCE LISTING

<110> Bayer HealthCare LLC  
Haaning, Jesper Mortensen  
Andersen, Kim Vilbour  
Ropke, Mads  
Glazer, Steven

<120> FVII or FVIIa Variants

<130> 0272wo310

<150> US 60/456,547

<151> 2003-03-20

<150> US 60/479,708

<151> 2003-06-19

<160> 21

<170> PatentIn version 3.5

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Ala  
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aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165  
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
5 10 15

aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp  
20 25 30

gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261  
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln  
35 40 45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309  
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu  
50 55 60 65

cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc 357  
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys  
70 75 80

gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc 405  
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly  
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acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn	549
gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys	597
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu	645
tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His	693
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly	741
gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val	789
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His	837
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His	885
gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu	933
gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp	981
cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu	1029
atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro	1077
aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys	1125
gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg	1173

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Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu	
370 375 380 385	
tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg	1317
Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu	
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35 40 45
Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
50 55 60
Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
65 70 75 80
Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
85 90 95
Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
100 105 110
Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
115 120 125
Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
130 135 140
Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145 150 155 160

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Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln  
 165 170 175  
 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala  
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 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu  
 195 200 205  
 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg  
 210 215 220  
 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn  
 225 230 235 240  
 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp  
 245 250 255  
 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr  
 260 265 270  
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 275 280 285  
 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg  
 290 295 300  
 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser  
 305 310 315 320  
 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser  
 325 330 335  
 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr  
 340 345 350  
 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys  
 355 360 365  
 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  
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 gcgccgggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa 180  
 agaggaacag tgcagctttg aggaagcccc ggagattttc aaagacgctg agcggaccaa 240  
 actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg 300  
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